

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: SHERMAN, Linda A.  
LUSTGARTEN, Joseph
- (ii) TITLE OF THE INVENTION: RECOMBINANT CONSTRUCTS ENCODING  
T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR  
ANTIGENS
- (iii) NUMBER OF SEQUENCES: 64
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: MORRISON & FOERSTER
  - (B) STREET: 2000 Pennsylvania Avenue, NW, suite 5500
  - (C) CITY: Washington
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20006-1888
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/812,393
  - (B) FILING DATE: 05-MAR-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Murashige, Kate H
  - (B) REGISTRATION NUMBER: 29,959
  - (C) REFERENCE/DOCKET NUMBER: 31333-20001.00
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 202-837-1500
  - (B) TELEFAX: 202-822-0168
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1350 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1233

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTC	GAG	ATG	CAG	AGG	AAC	CTG	GGA	GCT	GTG	CTG	GGG	ATT	CTG	TGG	GTG	48
Leu	Glu	Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val	
1				5					10					15		
CAG	ATT	TGC	TGG	CTG	AAA	GAA	TAG	CAA	GTG	CAG	CAG	AGT	CCC	GCA	TCC	96
Gln	Ile	Cys	Trp	Leu	Lys	Glu	Gln	Gln	Val	Gln	Gln	Ser	Pro	Ala	Ser	
			20						25					30		
TTG	GTT	CTG	CAG	GAG	GGG	GAG	AAC	GCA	GAG	CTC	CAG	TGT	AGC	TTT	TCC	144
Leu	Val	Leu	Gln	Glu	Gly	Glu	Asn	Ala	Glu	Leu	Gln	Cys	Ser	Phe	Ser	
			35					40					45			
ATC	TTT	ACA	AAC	CAG	GTG	CAG	TGG	TTT	TAC	CAA	CGT	CCT	GGG	GGA	AGA	192
Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg	
	50						55					60				
CTC	CTC	AGC	CTG	TTG	TAC	AAT	GCT	TCT	GGG	ACA	AAG	CAG	AGT	GGG	AGA	240
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg	
65					70					75				80		
CTG	ACA	TCC	ACA	ACA	GTG	ATT	AAA	GAA	GGT	GGG	AGC	TCT	TTG	CAC	ATT	288
Leu	Thr	Ser	Thr	Thr	Val	Ile	Lys	Glu	Arg	Arg	Ser	Ser	Leu	His	Ile	
				85						90				95		
TCC	TCC	TCC	CAG	ATC	ACA	GAC	TCA	GGC	ACT	TAT	CTC	TGT	GCC	TCA	AAT	336
Ser	Ser	Ser	Gln	Ile	Thr	Asp	Ser	Gly	Thr	Tyr	Leu	Cys	Ala	Ser	Asn	
			100					105					110			
TCT	GGA	GGA	AGC	AAT	GCA	AAG	CTA	ACC	TTC	GGG	AAA	GGC	ACT	AAA	CTC	384
Ser	Gly	Gly	Ser	Asn	Ala	Lys	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Lys	Leu	
			115				120					125				
TCT	GTT	AAA	TCA	GGT	GGC	GGA	GGG	TCT	GGC	GGG	GGT	GGA	TCC	GGG	GGT	432
Ser	Val	Lys	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	
		130					135					140				
GGA	GGC	TCA	GAG	GCT	GCA	GTG	ACC	CAA	AGC	CCA	AGA	AAC	AAG	GTG	GCA	480
Gly	Gly	Ser	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Asn	Lys	Val	Ala	
145					150					155				160		
GTA	ACA	GGA	GGA	AAG	GTG	ACA	TTG	AGC	TGT	AAT	CAG	ACT	AAT	AAC	CAC	528
Val	Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	Asn	Gln	Thr	Asn	Asn	His	
				165					170					175		
AAC	AAC	ATG	TAC	TGG	TAT	CGG	CAG	GAC	ACG	GGG	CAT	GGG	CTG	AGG	CTG	576
Asn	Asn	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Thr	Gly	His	Gly	Leu	Arg	Leu	
			180					185					190			
ATC	CAT	TAT	TCA	TAT	GGT	GCT	GGC	AGC	ACT	GAG	AAA	GGA	GAT	ATC	CCT	624
Ile	His	Tyr	Ser	Tyr	Gly	Ala	Gly	Ser	Thr	Glu	Lys	Gly	Asp	Ile	Pro	
			195				200					205				
GAT	GGA	TAC	AAG	GCC	TCC	AGA	CCA	AGC	CAA	GAG	AAC	TTC	TCC	CTC	ATT	672
Asp	Gly	Tyr	Lys	Ala	Ser	Arg	Pro	Ser	Gln	Glu	Asn	Phe	Ser	Leu	Ile	
	210					215						220				

CTG GAG TTG GCT ACC CCC TCT CAG ACA TCA GTG TAC TTC TGT GCG AGC	720
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser	
225 230 235 240	
GGT GAG ACA GGG ACC AAC GAA AGA TTA TTT TTC GGT CAT GGA ACC AAG	768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys	
245 250 255	
CTG TCT GTC CTG ACT AGT AAC TCC ATC ATG TAC TTC AGC CAC TTC CTG	816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val	
260 265 270	
CCG GTC TTC CTG CCA GGG AAG CCC ACC ACG ACG CCA GCG CCG CGA CAA	864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	
275 280 285	
CCA ACA CCG GCG CCC ACC ATC GCG TCG CAG CCC CTG TCC CTG CGC CAA	912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro	
290 295 300	
TCT AGT TCT AGA GAT CCC AAA CTC TGC TAC CTG CTG GAT GGA ATC CTC	960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu	
305 310 315 320	
TTC ATC TAT GGT GTC ATT CTC ACT GGC TTG TTC CTG AGA GTG AAG TTC	1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe	
325 330 335	
AGC AGG AGC GCA GAC GGC CCC GCG TAC CAG CAG GGC CAG AAC CAG CTC	1056
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu	
340 345 350	
TAT AAC GAG CTC AAT CTA GGA CGA AGA GAG GAG TAC GAT GTT TTG GAC	1104
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp	
355 360 365	
AAG AGA CGT GGC CGG GAC CCT GAG ATG GGG GGA AAG CCG AGA AGG AAG	1152
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys	
370 375 380	
AAC CCT CAG GAA GGC CTG TAC AAT GAA CTG CAG AAA GAT AAG ATG GCG	1200
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala	
385 390 395 400	
GAG GCC TAC AGT GAG ATT GGG ATG AAA GGC GAG CGC CGG AGG GGC AAG	1248
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys	
405 410 415	
GGG CAC GAT GGC CTT TAC CAG GGT CTC AGT ACA GGC ACC AAG GAC ACC	1296
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr	
420 425 430	
TAC GAC GCC CTT CAC ATG CAG GCC CTG CCC CCT CGC TAAGCGGCCG CCACCG	1344
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg	
435 440	
CG	1350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iv) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu	Glu	Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val
1				5					10					15	
Gln	Ile	Cys	Trp	Leu	Lys	Glu	Gln	Gln	Val	Gln	Gln	Ser	Pro	Ala	Ser
		20					25						30		
Leu	Val	Leu	Gln	Glu	Gly	Glu	Asn	Ala	Glu	Leu	Gln	Cys	Ser	Phe	Ser
		35				40						45			
Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg
	50					55					60				
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg
65					70					75				80	
Leu	Thr	Ser	Thr	Thr	Val	Ile	Lys	Glu	Arg	Arg	Ser	Ser	Leu	His	Ile
				85					90					95	
Ser	Ser	Ser	Gln	Ile	Thr	Asp	Ser	Gly	Thr	Tyr	Leu	Cys	Ala	Ser	Asn
			100					105					110		
Ser	Gly	Gly	Ser	Asn	Ala	Lys	Leu	Thr	Phe	Gly	Lys	Gly	Thr	Lys	Leu
		115					120					125			
Ser	Val	Lys	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
	130				135						140				
Gly	Gly	Ser	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Asn	Lys	Val	Ala
145					150					155				160	
Val	Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	Asn	Gln	Thr	Asn	Asn	His
			165						170					175	
Asn	Asn	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Thr	Gly	His	Gly	Leu	Arg	Leu
		180					185						190		
Ile	His	Tyr	Ser	Tyr	Gly	Ala	Gly	Ser	Thr	Glu	Lys	Gly	Asp	Ile	Pro
	195						200					205			
Asp	Gly	Tyr	Lys	Ala	Ser	Arg	Pro	Ser	Gln	Glu	Asn	Phe	Ser	Leu	Ile
	210				215						220				
Leu	Glu	Leu	Ala	Thr	Pro	Ser	Gln	Thr	Ser	Val	Tyr	Phe	Cys	Ala	Ser
225					230					235					240
Gly	Glu	Thr	Gly	Thr	Asn	Glu	Arg	Leu	Phe	Phe	Gly	His	Gly	Thr	Lys
			245						250					255	
Leu	Ser	Val	Leu	Thr	Ser	Asn	Ser	Ile	Met	Tyr	Phe	Ser	His	Phe	Val
		260						265					270		
Pro	Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro
	275						280					285			
Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg	Pro
	290					295					300				
Ser	Ser	Ser	Arg	Asp	Pro	Lys	Leu	Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu
305					310					315					320
Phe	Ile	Tyr	Gly	Val	Ile	Leu	Thr	Ala	Leu	Phe	Leu	Arg	Val	Lys	Phe
			325						330					335	
Ser	Arg	Ser	Ala	Asp	Ala	Pro	Ala	Tyr	Gln	Gln	Gly	Gln	Asn	Gln	Leu
		340						345					350		
Tyr	Asn	Glu	Leu	Asn	Leu	Gly	Arg	Arg	Glu	Glu	Tyr	Asp	Val	Leu	Asp
	355					360						365			
Lys	Arg	Arg	Gly	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Pro	Arg	Arg	Lys
	370					375					380				

Asn	Pro	Gln	Glu	Gly	Leu	Tyr	Asn	Glu	Leu	Gln	Lys	Asp	Lys	Met	Ala
385					390					395					400
Glu	Ala	Tyr	Ser	Glu	Ile	Gly	Met	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys
			405						410					415	
Gly	His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr
		420					425						430		
Tyr	Asp	Ala	Leu	His	Met	Gln	Ala	Leu	Pro	Pro	Arg				
	435					440									

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: V-alpha-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCAAGGCAC TGATGTTTCAAT CTTC

24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: V-alpha-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGAGACAAAG TCCCAATCT CTGACAG

27

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: V-alpha-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGCAGCTGC TCCTCAAGTA CTATTC

26

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-4.1.2.3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCCCGGAGAA GGTCCACAGT TCTCTTT

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-4.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGCAGCAG AGGTTTGAA GGCACATAC

29

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGCAGGTCTT CACTTCTTTA TGAAGGT

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGTTCCTCTT CAGGTCACG AATATGT

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGAAGAAGACT CAGCCTGGAC TGTTCAT

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCTCCACA GAAACAAGA GGACCGAGCA

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGCTGCGAC GTTCCTTAGT GACTGTG

27

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCGTCAGC CTGTTGTCCA ATCCTTCTGS

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAGCCTCATC AATCTGTTCT ACTTGCT

28

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACCAGGGA CCACAGTTTA TCATTCAA

28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACCTGGAGAG AATCCTAAGC TCATCAT

27

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTCTTGTS TCCTGACAG TCCTGGTT

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAAGCAAACA CTGTASTGCA GAGCCCTTCC

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAGACATCC ATAAGTGCCC TACAG

35

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTGTATGAAA CCCAGGACAG TTCTTAC

27

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGTATTTCT TTCTTATGTT GTTTTGGAT

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-alpha-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CAAAGCTCTC CATCGCTGAC TGTTC AAG

28

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATCTAATCCT GCGAAGAGCA AAT

23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCGTCTGGT ACCACGTGGT CAA

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTGAAAGGGC AAGGACAAAA AGC

23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATGCGAA CACTATCTAG GT

22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-5.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ACATAATCAA AGGAAAGGGA GAA

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCCTGATTGG TCAGGAAGGG CAA

23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TACCTGATCA AAAGAATGGG AGA

23

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-8.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATAACCATGA CAATATGTAC TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-8.2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATAACCACAA CAACATGTAC TGG

23

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-8.3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATAGCCACAA CTACATGTAC TGG

23

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCTTGCAAG AGTTGCAAAA CCA

23

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATTATGTTT AGCTACAATA ATA

23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACAAGGTGAC AGGGAAGGGA CAA

23

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACCTACAGAA CCCAAGGACT CAG

23

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGTTGCCCT CGGATCGATT TTC

23

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCCGAGATCA AAGCTGTGG CAG

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGAACCATCT GTAAGAGTGG AAC

23

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CATCAAATAA TAGATATGGG GCA

23

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTAGTCCTGA AAAAGGGCAC ACT

23

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: V-beta-18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CATCTGTCAA AGTGGTACTT CA

22

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...393

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATG AAA TCC TTG AGT GTT TCC CTA GTG GTC CTC TGG CTC CAG TTA AAC	48
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn	
1 5 10 15	
TGG GTG CAG AGC CAG CAG AAG GTG CAG CAG AGC CCA GAA TCC CTC AGT	96
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser	
20 25 30	
GTC CCA GAG GGA GGC ATG GGC TCT CTC AAC TGC ACT TCA AGT GAT CGC	144
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg	
35 40 45	
AAT TTT CAG TAT TTC TGG TGG TAC AGA CAG CAT TCT GGA GAA GGC CCC	192
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro	
50 55 60	
AAA GCA CTG ATG TCC ATC TTC TCT GAT GGT GAC AAG AAA GAA GGC AGA	240
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg	
65 70 75 80	
TTC ACA GCT CAC CTC AAT AAG GGC AGC CTG CAT GTT TCC CTG CAC ATC	288
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile	
85 90 95	
AGA GAC TCC CAG CCC AGT GAC TCC GCT CTC TAC TTC TGT GCA GTT ATG	336
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met	
100 105 110	
GAT TAT AAC CAG GGG AAG CTT ATC TTT GGG CAG GGT ACC AAG TTA TCT	384
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser	
115 120 125	
ATC AAG CCC	393
Ile Lys Pro	
130	

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
 1           5           10           15
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
          20           25           30
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
          35           40           45
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
 50           55           60
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
65           70           75           80
Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
          85           90           95
Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
          100          105          110
Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
          115          120          125
Ile Lys Pro
          130

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...402
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

ATG GGC TCC AGA CTC TTC TTT GTG GTT TTG ATT CTC CTG TGT GCA AAA      48
Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys
 1           5           10           15

CAC ATG GAG GGT GCA GTC ACC CAA AGT CCA AGA AGC AAG GTG GCA GTA      96
His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val
          20           25           30

ACA GGA GGA AAG GTG ACA TTG AGC TGT CAC CAG ACT AAT AAC CAT GAC      144
Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp

```



35	40	45	
TAT ATG TAC TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC	192		
Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile			
50	55	60	
CAT TAC TCA TAT GTC GGT GAC AGC ACG GAG AAA GGA GAT ATC CCT GAT	240		
His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp			
65	70	75	80
GGG TAC AAG GCG TCC AGA CCA AGC CAA GAG AAT TTC TCT CTC ATT CTG	288		
Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu			
85	90	95	
GAG TTG GGT TCC CTT TCT CAG TCA GGT GTA TAT TTC TGT GCG AGC AGC	336		
Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser			
100	105	110	
GAT TTC GGC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT CCC GGC	384		
Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly			
115	120	125	
ACC AGG CTC ACG GTT TCT	402		
Thr Arg Leu Thr Val Ser			
130			

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys	
1	15
His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val	
20	30
Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp	
35	45
Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile	
50	60
His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp	
65	80
Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu	
85	95
Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser	
100	110
Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly	
115	125
Thr Arg Leu Thr Val Ser	
130	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Ile Phe Gly Ser Leu Ala Phe Leu  
1 9

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu  
1 10

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Val Met Ala Gly Val Gly Ser Pro Tyr Val  
1 10

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Val Leu Gln Gly Leu Pro Arg Glu Tyr Val  
1 10

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His Leu Tyr Gln Gly Gln Trp  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Arg Leu Leu Gln Glu Thr Glu Leu Val  
1 5

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Ile Pro Val Ala Ile Lys Val Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Cys Leu Thr Ser Thr Val Gln Leu Val  
1 5

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Leu Met Pro Tyr Gly Cys Leu Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Val Leu Val Lys Ser Pro Asn His Val  
1 5

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Asp Ile Asp Glu Thr Glu Tyr His Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Leu Leu Glu Lys Gly Glu Arg Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Glu Leu Val Ser Glu Phe Ser Arg Met  
1 5

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Glu Leu Val Ser Glu Phe Ser Arg Met Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Leu Val Ser Glu Phe Ser Arg Met Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Leu Val Asp Ala Glu Glu Tyr Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Leu Ser Pro Gly Lys Asn Gly Val  
1 5

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Lys Leu Val Gly Lys Leu Asn Trp Ala  
1 5